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Presentation of the Madbot project

Imane Messak

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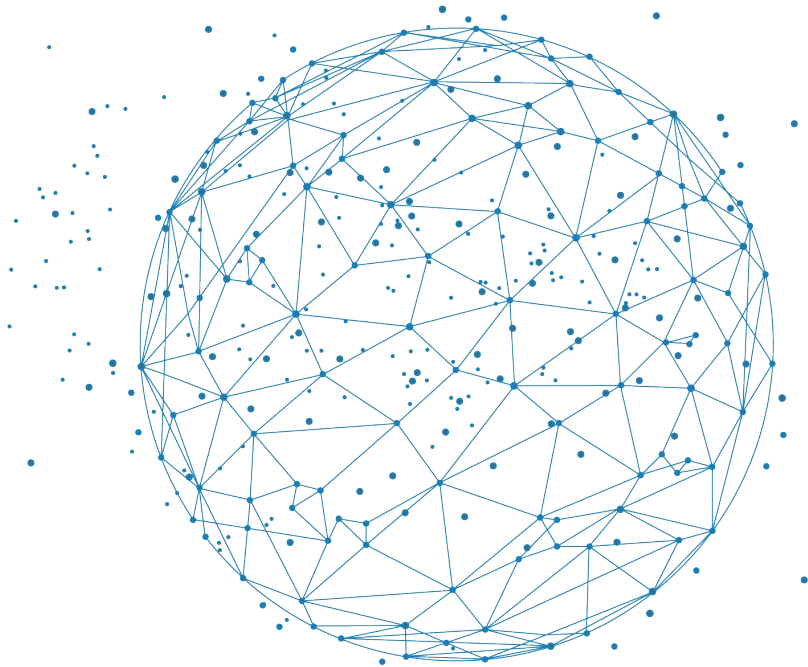
Submitted on 13 May 2025

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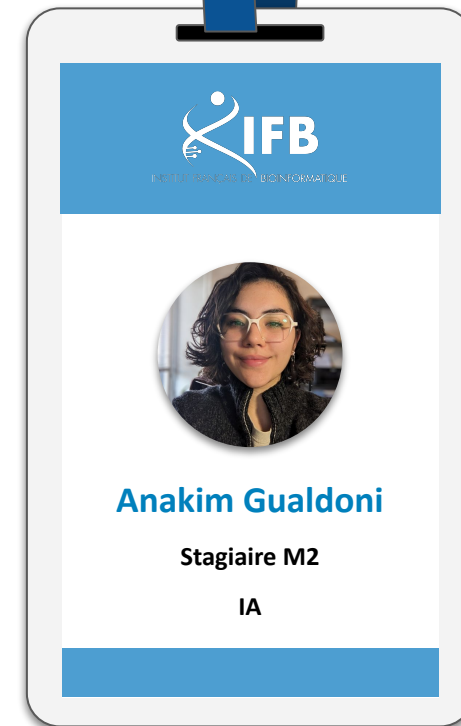
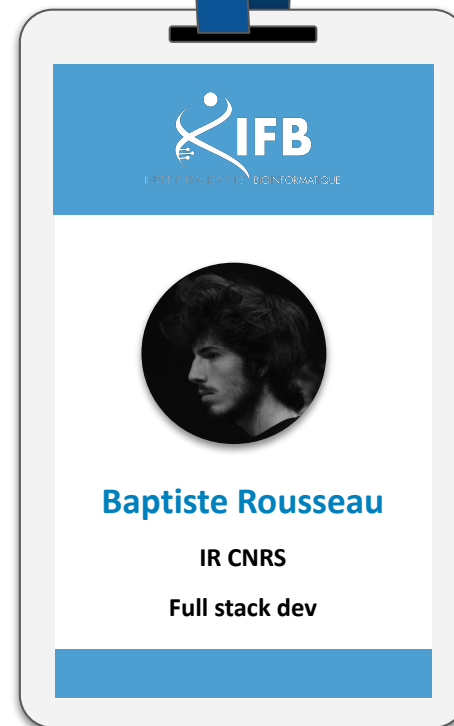
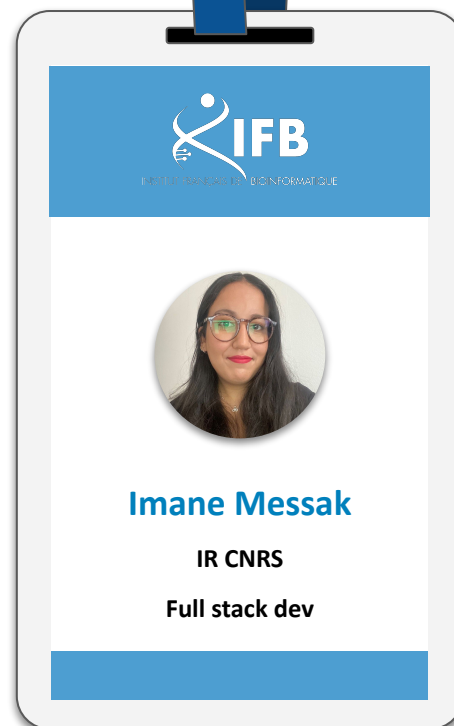
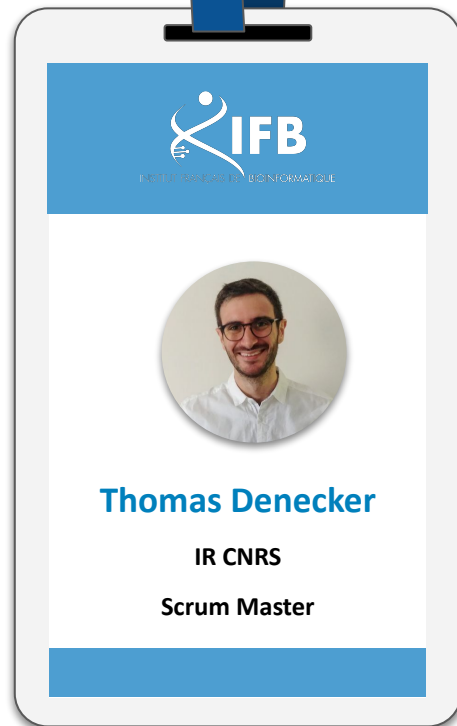


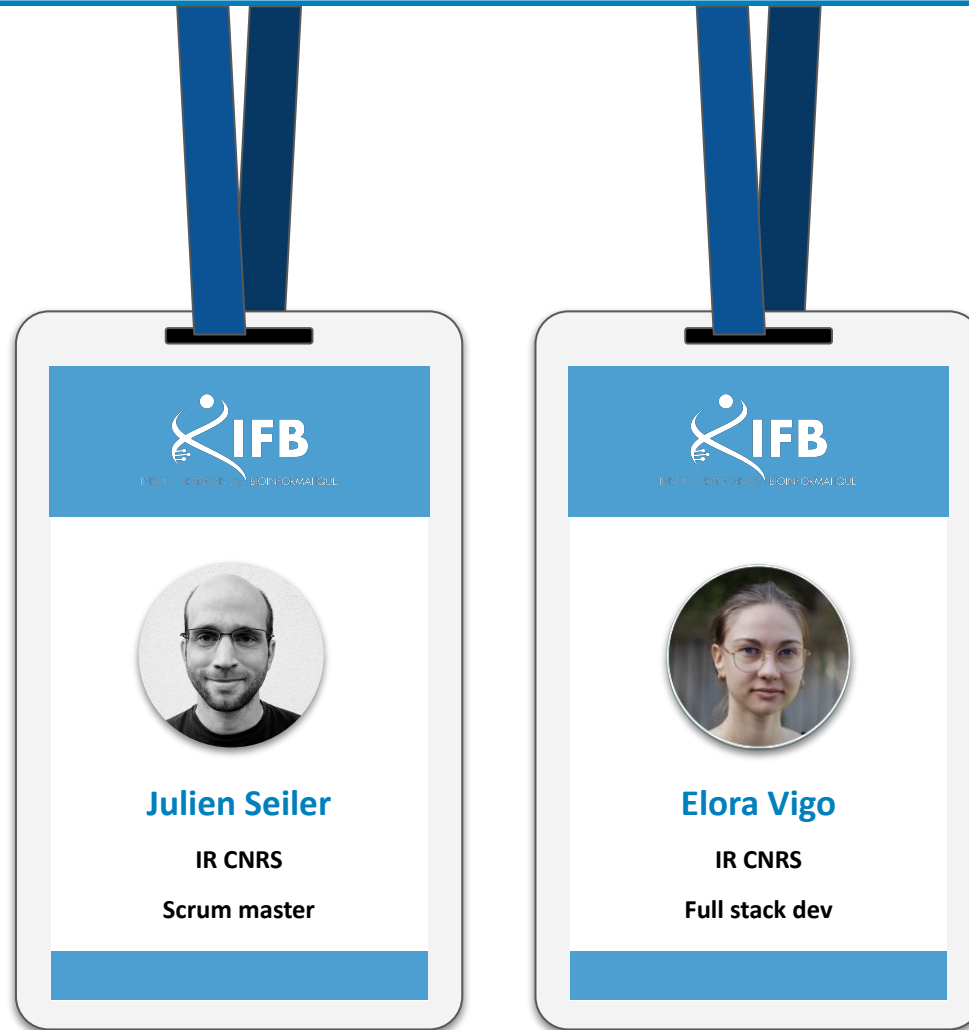
MADBOT

Metadata And Data Brokering Online Tool

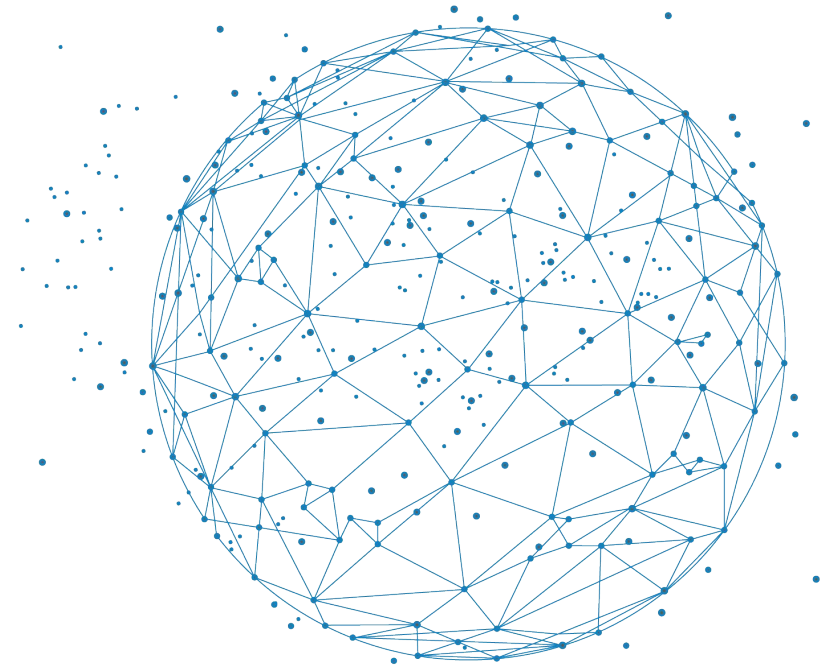
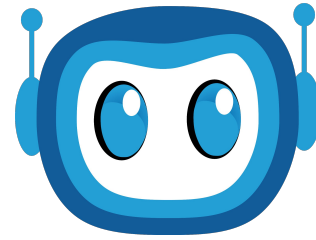
MESSAK Imane
0000-0002-1654-6652 

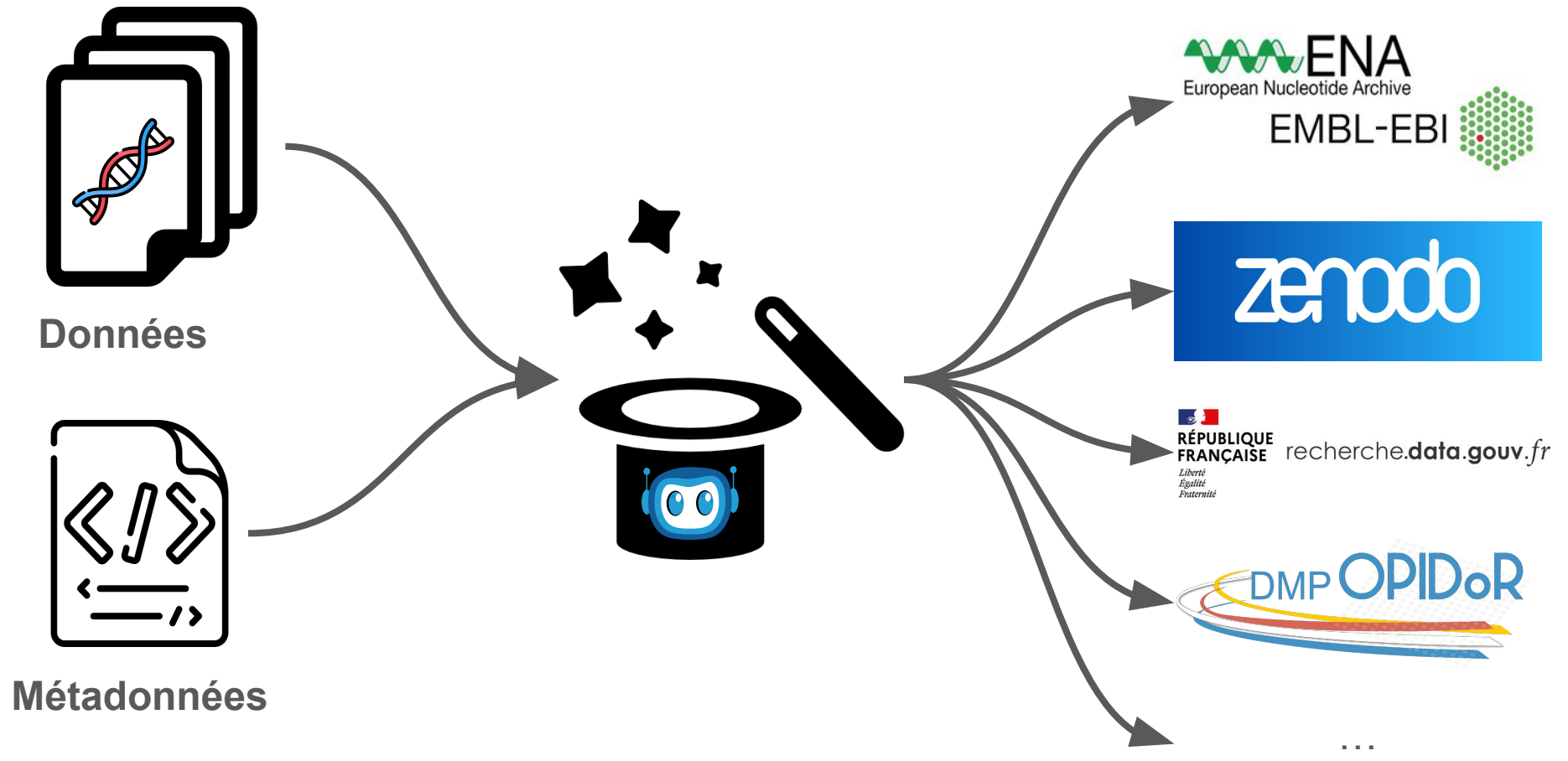
L'équipe MADBOT Paris





C'est quoi MADBOT?







MADBOT (Metadata And Data Brokering Online Tool) est une application web qui fournit **un tableau de bord pour la gestion des données et des métadonnées de recherche.**

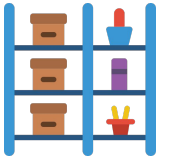


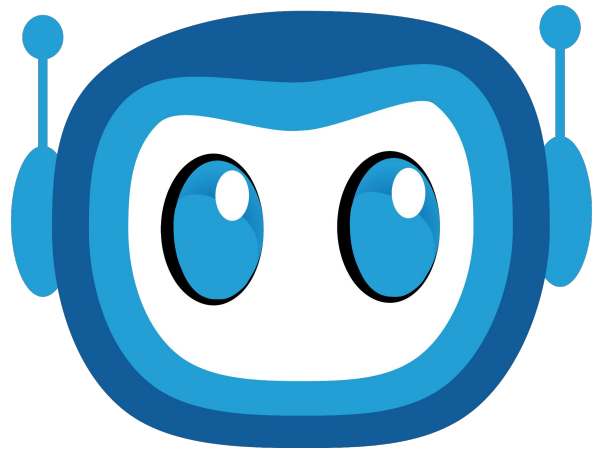


MADBOT (Metadata And Data Brokering Online Tool) est une application web qui fournit **un tableau de bord pour la gestion des données et des métadonnées de recherche.**



L'application permet d'**agréger les métadonnées** autour de projets scientifiques et d'**identifier précisément où sont stockées les données** au travers de nombreux connecteurs.

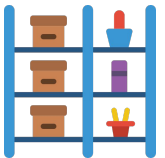




MADBOT (Metadata And Data Brokering Online Tool) est une application web qui fournit **un tableau de bord pour la gestion des données et des métadonnées de recherche.**



L'application permet d'**agrég**er les **métadonnées** autour de projets scientifiques et d'**identifier précisément où sont stockées les données** au travers de nombreux connecteurs.



Elle accompagne également les chercheurs pour la **publication des données et des métadonnées** vers un grand nombre d'entrepôts généraliste (RGD, Zenodo, etc.) et thématique (ENA, GEO, etc.)



Pourquoi un MVP ? Notre feuille de route

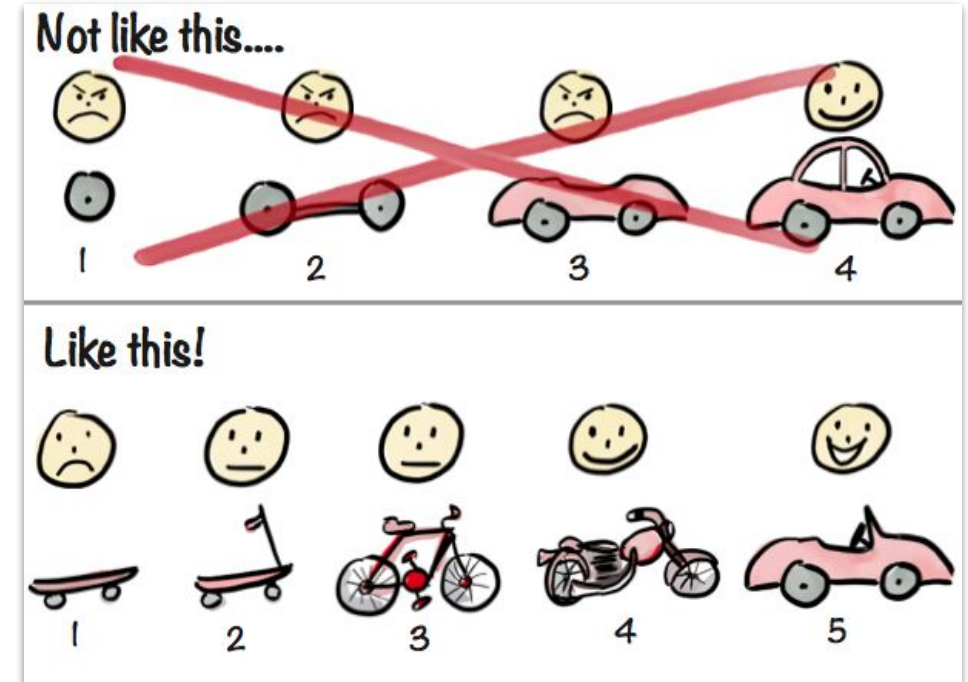


Nous souhaitons produire le plus rapidement possible une application fonctionnelle.

Objectifs principaux

- Démontrer que nous pouvons associer à un arbre ISA des données localisées sur différents systèmes de stockage (Galaxy et SSHFS)
- Démontrer que nous pouvons renseigner des métadonnées pour un arbre ISA et ses données
- Démontrer que nous pouvons publier ces données sur des entrepôts de références thématiques (ENA) et non thématiques (Zenodo).

L'application MADBOT capable de réaliser ces objectifs est notre **Minimal Viable Product (MVP)**.



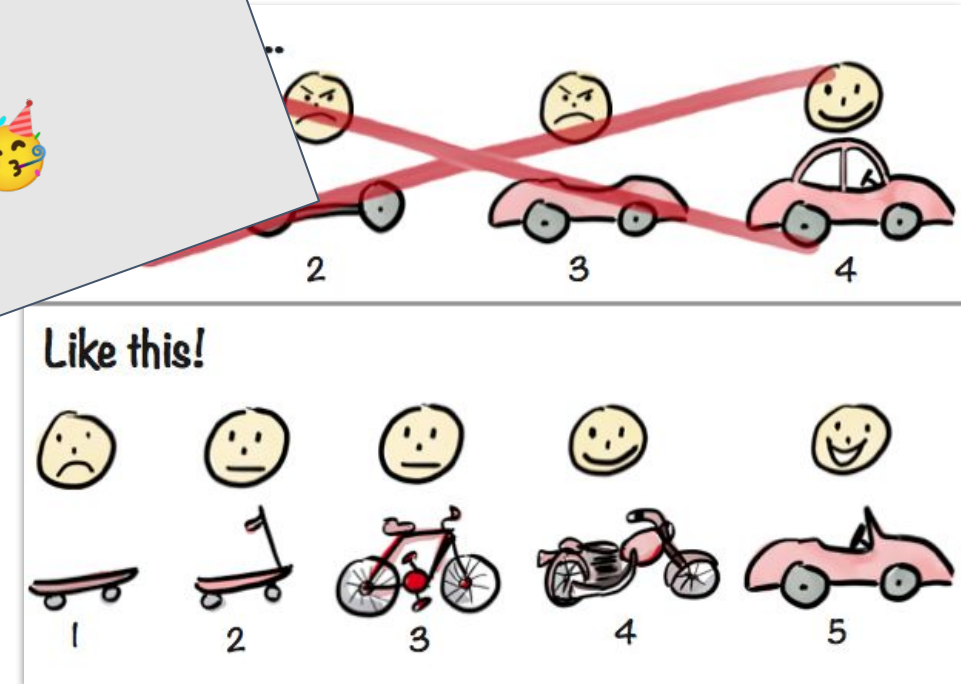


Nous souhaitons produire le plus rapidement possible une application fonctionnelle.

Objectifs principaux

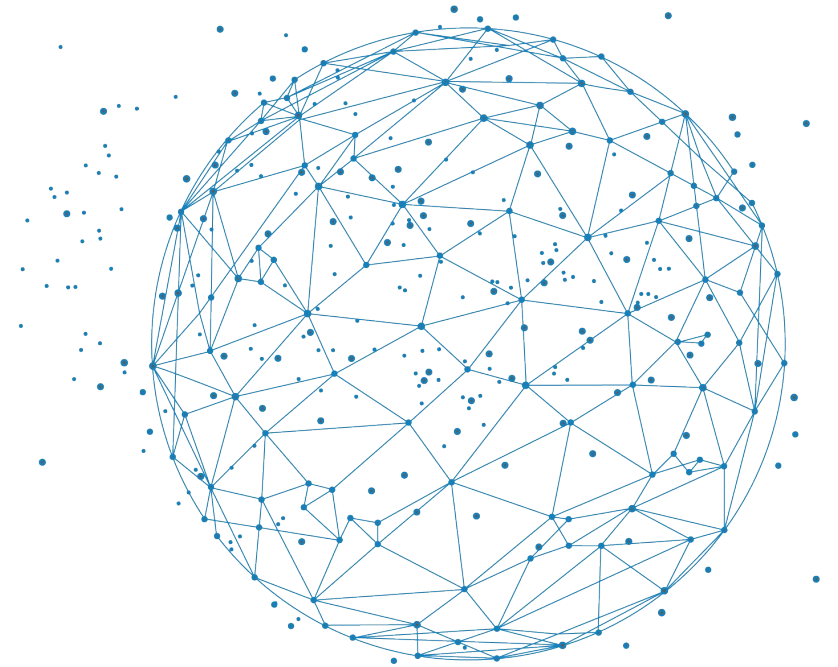
- Démontrer que nous pouvons associer à un arbre des données localisées sur différents systèmes (Galaxy et SSHFS)
- Démontrer que nous pouvons générer un arbre ISA et...
- Démontrer que nous pouvons générer des entrepôts de référence sur des thématiques (Zenodo) et non

Mission MVP accomplie 🎉



L'application MADBOT capable de réaliser ces objectifs est notre Minimal Viable Product (MVP).

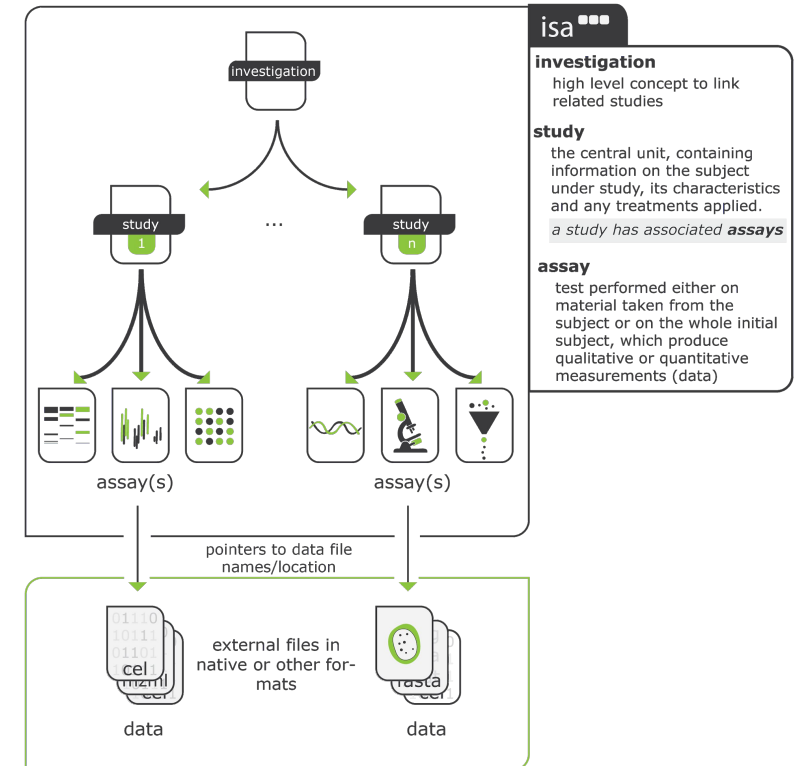
Comment ça fonctionne ?





Au sein de **MADBOT**, chaque projet de recherche est décrit sous la forme d'un ensemble de **Nodes** qui peuvent être des **investigations**, des **études (study)** et des **expériences (assay)**, cela sous la forme d'un arbre hiérarchique (modèle ISA). Ces ensembles de **Nodes** sont regroupés dans des workspaces.

- **Investigation** : le contexte du projet
- **Study** : une expérimentation en un seul lieu
- **Assay** : une mesure spécifique qui cible un trait avec une méthode et une échelle.



Sources : <https://isa-tools.org> et <https://isa-specs.readthedocs.io/en/latest/isamodel.html>



Mais nous ne nous limitons pas qu'au modèle ISA et nous prévoyons de mettre en place de nouvelles collections de type de *Nodes*.

Chaque élément de cet arbre peut être associés à des données, des échantillons biologiques et des métadonnées.





MADBOT ☰

⚙️ Parameters

Welcome to Madbot

Madbot allows you to identify and track the data and metadata associated with the different stages of your research projects.

To get started, you need to create at least one workspace.
A workspace lets you organize your work as you wish, for yourself, your team or an entire organization.

A workspace name is required to start.

START

Imane Messak ↔



MADBOT ☰

⚙️ Parameters

Welcome to Madbot

Madbot allows you to identify and track the data and metadata associated with the different stages of your research projects.

To get started, you need to create at least one workspace.
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Workspace name
my team workspace

START

CLICK!

Imane Messak ↔




MADBOT ☰


MY TEAM WORKSPACE ▼

- Dashboard
- Inbox
- Parameters
- Submissions
- New investigation** CLICK!

Dashboard



No datalinks found
It's time to link some data!

Create your first node and go to the Datalinks tab to identify where your data are located. 

[NEW INVESTIGATION](#)

Imane Messak ↗ ?

Création d'un Node Investigation



The screenshot shows the MADBOT web interface. On the left is a sidebar with a menu: Dashboard, Inbox, Parameters, Submissions, New investigation, and an expanded 'Untitled' section. The main area is titled 'Untitled' and contains the text 'investigation' and 'Choose how to create this investigation...'. Two options are listed: 'EMPTY INVESTIGATION' and 'DEMO INVESTIGATION'. A yellow arrow points to the 'DEMO INVESTIGATION' option with the text 'CLICK!' written next to it. At the top right of the main area, it says 'Everything saved'. At the bottom left, the user 'Imane Messak' is logged in. At the bottom right, there is a help icon (question mark).



MADBOT

MY TEAM WORKSPACE

- Dashboard
- Inbox
- Parameters
- Submissions
- New investigation

▼ **Growth control of the eukaryot...**

- > A time course analysis of tran...
- > Study of the impact of change...

Growth control of the eukar... Everything saved

Growth control of the eukaryote cell: a systems biology study in yeast

investigation

Background Cell growth underlies many key cellular and developmental processes, yet a limited number of studies have been carried out on cell-growth regulation. Comprehensive studies at the transcriptional, proteomic and metabolic levels under defined controlled conditions are currently lacking. Results Metabolic control analysis is being exploited in a systems biology study of the eukaryotic cell. Using chemostat culture, we have measured the impact of changes in flux (growth rate) on the transcriptome, proteome, endometabolome and exometabolome of the yeast *Saccharomyces cerevisiae*. Each functional genomic level shows clear growth-rate-associated trends and discriminates between carbon-sufficient and carbon-limited conditions. Genes consistently and significantly upregulated with increasing growth rate are frequently essential and encode evolutionarily conserved proteins of known function that participate in many protein-protein interactions. In contrast, more unknown, and fewer essential, genes are downregulated with increasing growth rate; their protein products rarely interact with one another. A large proportion of yeast genes under positive growth-rate control share orthologs with other eukaryotes, including humans. Significantly, transcription of genes encoding components of the TOR complex (a major controller of eukaryotic cell growth) is not subject to growth-rate regulation. Moreover, integrative studies reveal the extent and importance of post-transcriptional control, patterns of control of metabolic fluxes at the level of enzyme synthesis, and the relevance of specific enzymatic reactions in the control of metabolic fluxes during cell growth. Conclusion This work constitutes a first comprehensive systems biology study on growth-rate control in the eukaryotic cell. The results have direct implications for advanced studies on cell growth, in vivo regulation of metabolic fluxes for comprehensive metabolic engineering, and for the design of genome-scale systems biology models of the eukaryotic cell.

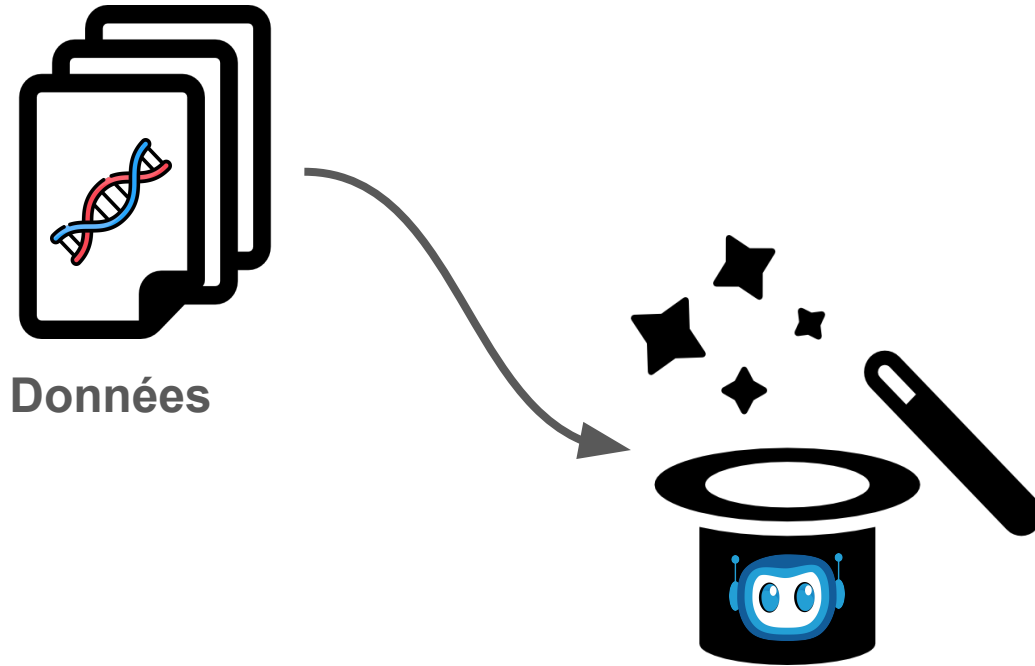
DATALINKS 0 SAMPLES 0 METADATA 0 STUDY 2

NEW DATALINK

Name	Connections	Data access
No data available		

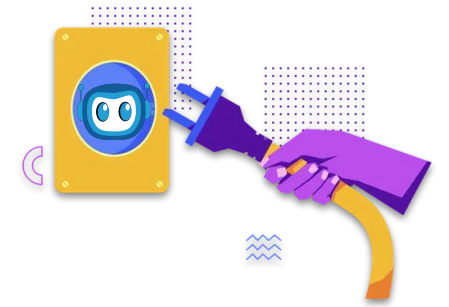
Items per page: 10 0-0 of 0 < >

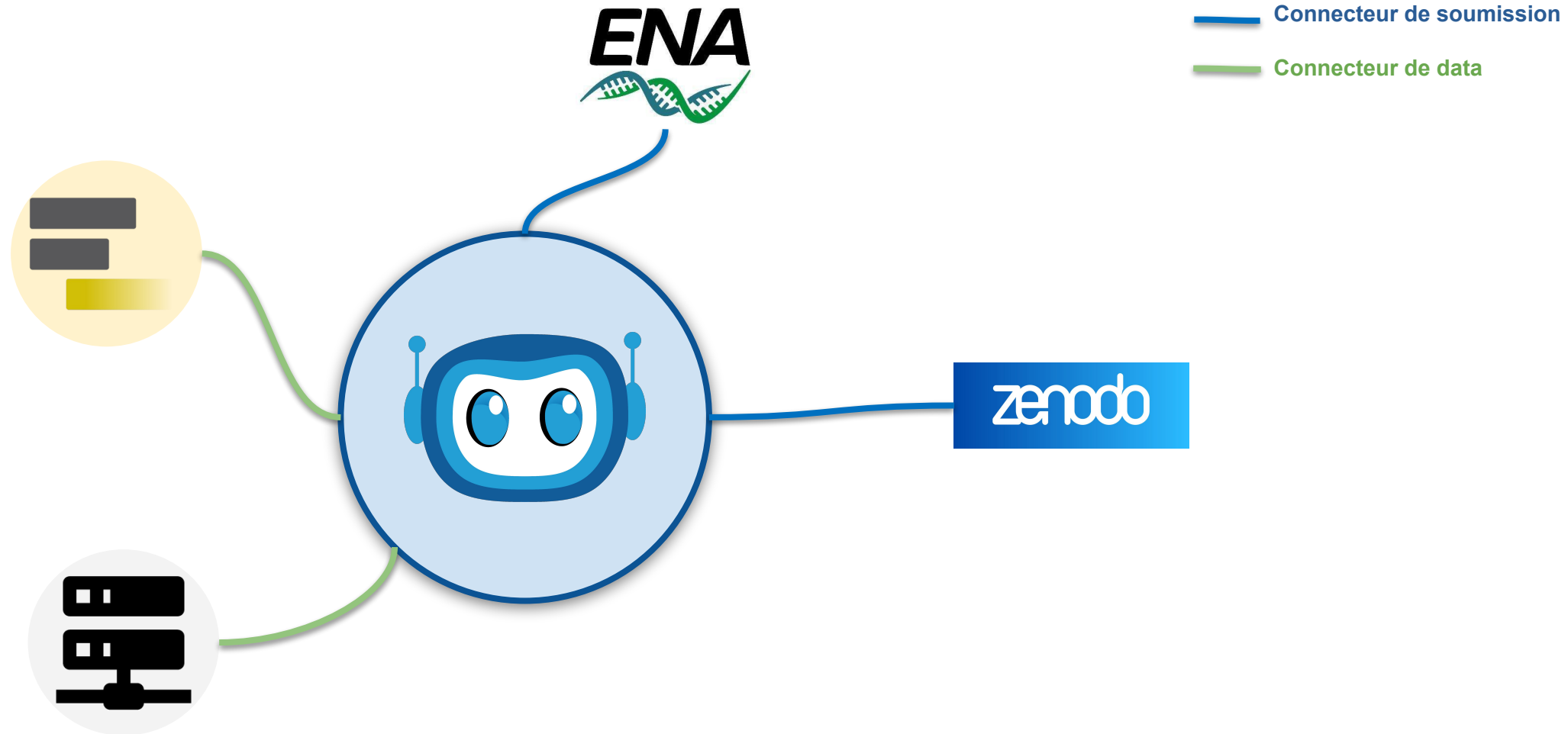
Imane Messak

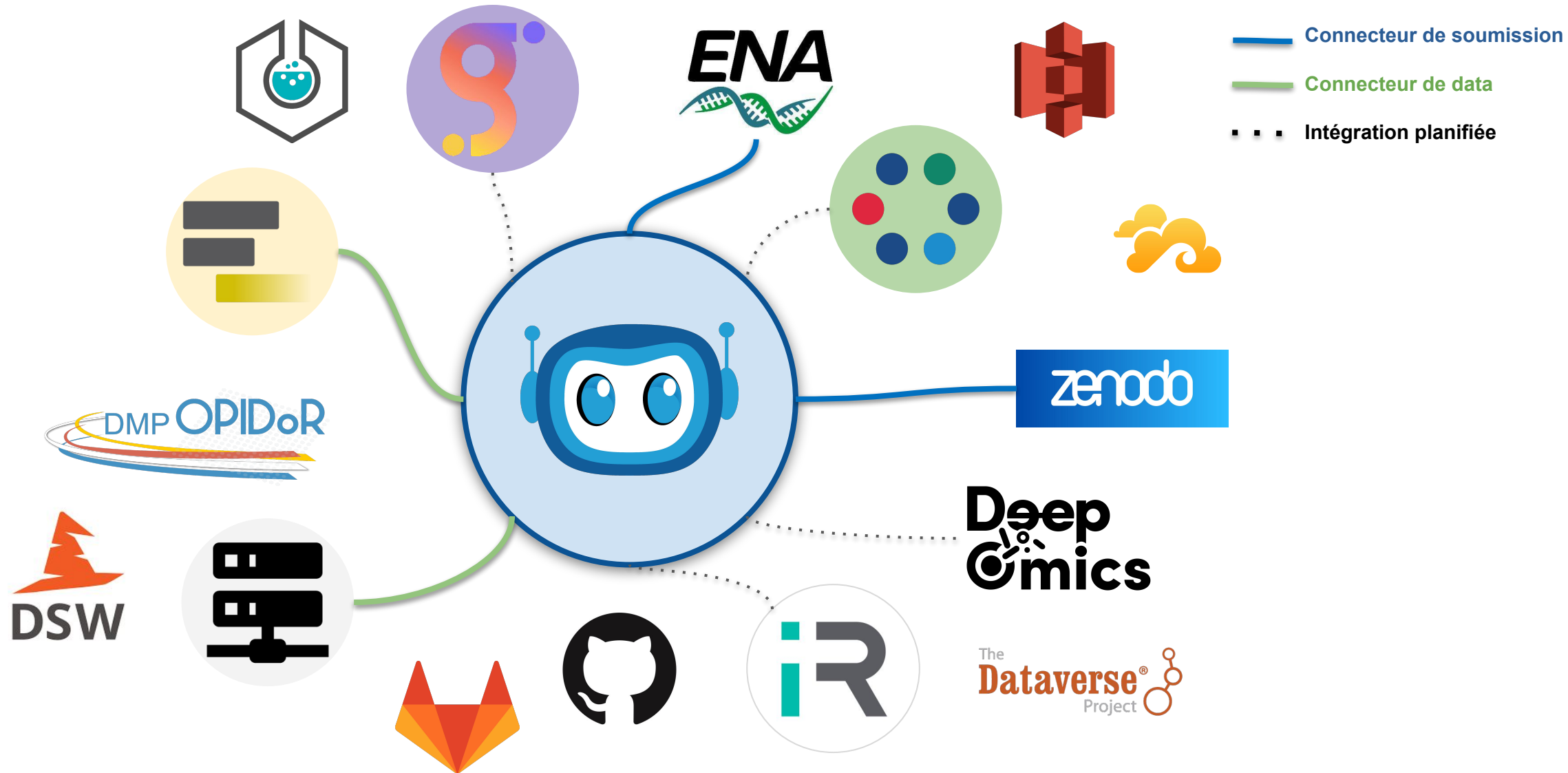


Les connecteurs sont des modules Python permettant d'accéder aux données d'**outils de gestion de données**, tels que Galaxy, via leurs API.

Conçus de manière **modulaire**, les connecteurs de MADBOT permettent à chacun de **contribuer en développant de nouveaux connecteurs** adaptés à ses besoins.

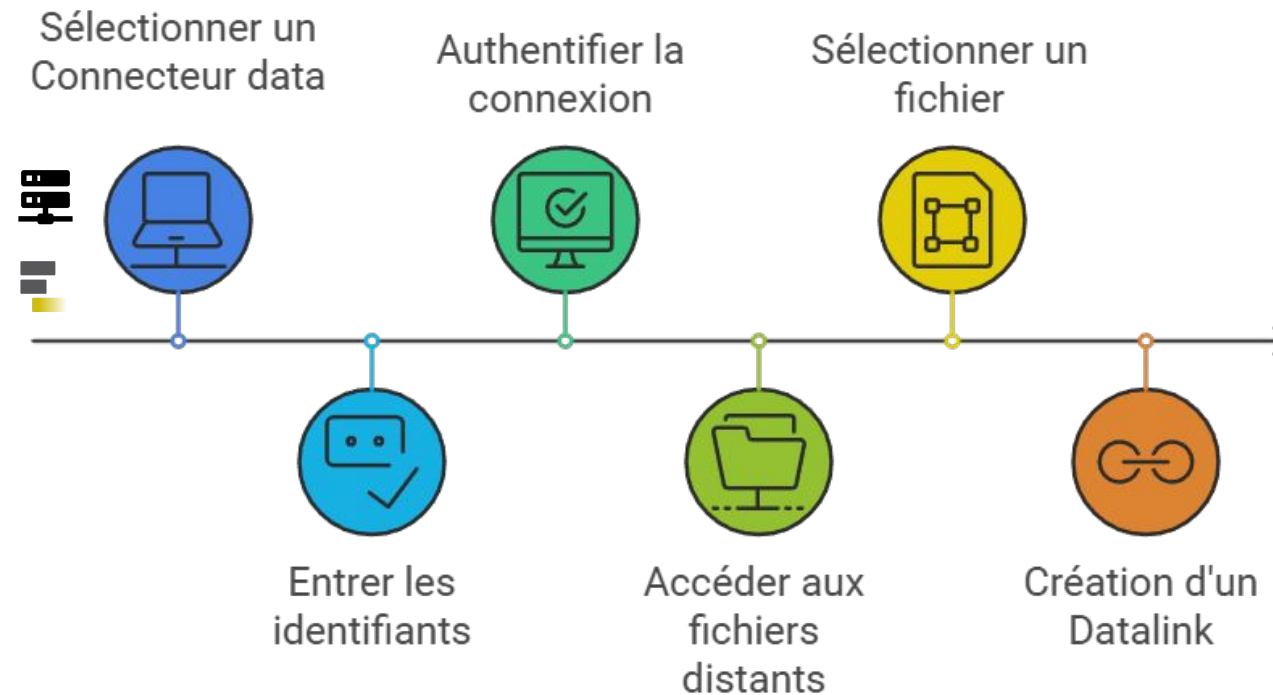








Un datalink est un **lien** entre **une donnée accessible à distance** via un connecteur et un **Node**.
Ainsi, **aucun fichier n'est stocké en local**.





The screenshot shows the MADBOT web interface. On the left is a navigation sidebar with options: Dashboard, Inbox (10), Parameters, Submissions, and New investigation. The main content area displays the title 'Growth control of the eukaryote cell: a systems biology study in yeast' and a detailed background text about cell growth regulation in yeast. Below the text are tabs for 'DATALINKS 1', 'SAMPLES 1', 'METADATA 3', and 'STUDY 1'. A table with columns 'Name', 'Connections', and 'Data access' is shown, but it contains 'No data available'. A yellow arrow points to a 'NEW DATALINK' button with the text 'CLICK!' next to it. At the bottom left, the user 'Imane Messak' is logged in. At the bottom right, there is a '1-1 of 1' indicator and navigation arrows.



MADBOT beta

DEMO - YEAST GROWTH CONTROL ...

Dashboard
Inbox
Parameters
Submissions
New investigation

Growth control of the eukaryote cell: a systems biology study in yeast

Everything saved

Add a datalink

1 Choose a connector 2 Connect 3 Select a data

Choose an existing connection

- Galaxy
Galaxy France Demo
- SSHFS
core.cluster.france-bioinformatique.fr

No more items

Create a new connection from a connector

- Galaxy
- SSHFS

or

NEW DATALINK

1-1 of 1

Imane Messak



MADBOT beta

DEMO - YEAST GROWTH CONTROL ...

Dashboard
Inbox
Parameters
Submissions
New investigation

Growth control of the eukaryote cell: a systems biology study in yeast

Everything saved

Growth control of the eukaryote cell: a systems biology study in yeast

Comprehensive studies at the systems biology study of the eukaryotic cell of the yeast *Saccharomyces cerevisiae* have shown that genes consistently and significantly interact with each other. In contrast, more genes under positive growth-rate control (of eukaryotic cell growth) are not regulated at the level of enzyme synthesis, but rather at the level of gene expression. This systems biology study on growth-rate control is relevant for metabolic engineering, and for the design of synthetic biological systems.

Add a datalink

1 Choose a connector 2 Connect 3 Select a data

Complete the form below to connect to Galaxy

Shared parameters

Galaxy Instances

Url Galaxy

is a required property

Private parameters

Login*

is a required property

Password*

is a required property

BACK CONNECT

NEW DATALINK

1-1 of 1

Imane Messak



ADD A DATALINK

1 Choose a connector 2 **Connect** 3 Select a data

Complete the form below to connect to Galaxy

Shared parameters

Galaxy Instances

Url Galaxy
Galaxy France

The Galaxy platforms.

Private parameters

Login*
imane.messak@france-bioinformatique.fr

The username or email address used for authentication.

Password*
.....

The user's password, which must be kept confidential.

BACK CONNECT **CLICK!**



MADBOT beta Growth control of the eukar... Everything saved

DEMO - YEAST GROWTH CONTROL ...

Dashboard
Inbox
Parameters
Submissions
New investigation

Growth control of the eukaryote cell: a systems biology study in yeast

Add a datalink

1 Choose a connector 2 Connect 3 Select a data

All histories/

- > test_empty_history
- > NC_0445512.2 reference sequence
- > Assembly
- > Imaging
- > COVID ressources
- > assembly and chipseq
- > fasta NC_045512.2 reference sequence **CLICK!**
- > covid test data

Galaxy
Galaxy France

Selected data

BACK CREATE DATALINK (0)

NEW DATALINK

1-1 of 1 |< < > >|

Imane Messak



MADBOT beta

DEMO - YEAST GROWTH CONTROL ...

Dashboard
Inbox
Parameters
Submissions
New investigation

Growth control of the eukaryote cell: a systems biology study in yeast

Everything saved

Add a datalink

1 Choose a connector Connect 3 Select a data

All histories/ fasta NC_045512/

UNSELECT ALL LINKABLE DATA

NC_045512.2.fasta

Galaxy
Galaxy France

NC_045512.2.fasta
Galaxy Dataset

Selected data

NC_045512.2.fasta

CLICK!

NEW DATALINK

1-1 of 1

Imane Messak



MADBOT beta

DEMO - YEAST GROWTH CONTROL ...

- Dashboard
- Inbox 10
- Parameters
- Submissions
- New investigation

✓ **Growth control of the eukaryote cell: a ...**

- Study of the impact of changes in fl...

Growth control of the eukar... Everything saved

Growth control of the eukaryote cell: a systems biology study in yeast

investigation

Background Cell growth underlies many key cellular and developmental processes, yet a limited number of studies have been carried out on cell-growth regulation. Comprehensive studies at the transcriptional, proteomic and metabolic levels under defined controlled conditions are currently lacking. Results Metabolic control analysis is being exploited in a systems biology study of the eukaryotic cell. Using chemostat culture, we have measured the impact of changes in flux (growth rate) on the transcriptome, proteome, endometabolome and exometabolome of the yeast *Saccharomyces cerevisiae*. Each functional genomic level shows clear growth-rate-associated trends and discriminates between carbon-sufficient and carbon-limited conditions. Genes consistently and significantly upregulated with increasing growth rate are frequently essential and encode evolutionarily conserved proteins of known function that participate in many protein-protein interactions. In contrast, more unknown, and fewer essential, genes are downregulated with increasing growth rate; their protein products rarely interact with one another. A large proportion of yeast genes under positive growth-rate control share orthologs with other eukaryotes, including humans. Significantly, transcription of genes encoding components of the TOR complex (a major controller of eukaryotic cell growth) is not subject to growth-rate regulation. Moreover, integrative studies reveal the extent and importance of post-transcriptional control, patterns of control of metabolic fluxes at the level of enzyme synthesis, and the relevance of specific enzymatic reactions in the control of metabolic fluxes during cell growth. Conclusion This work constitutes a first comprehensive systems biology study on growth-rate control in the eukaryotic cell. The results have direct implications for advanced studies on cell growth, in vivo regulation of metabolic fluxes for comprehensive metabolic engineering, and for the design of genome-scale systems biology models of the eukaryotic cell.

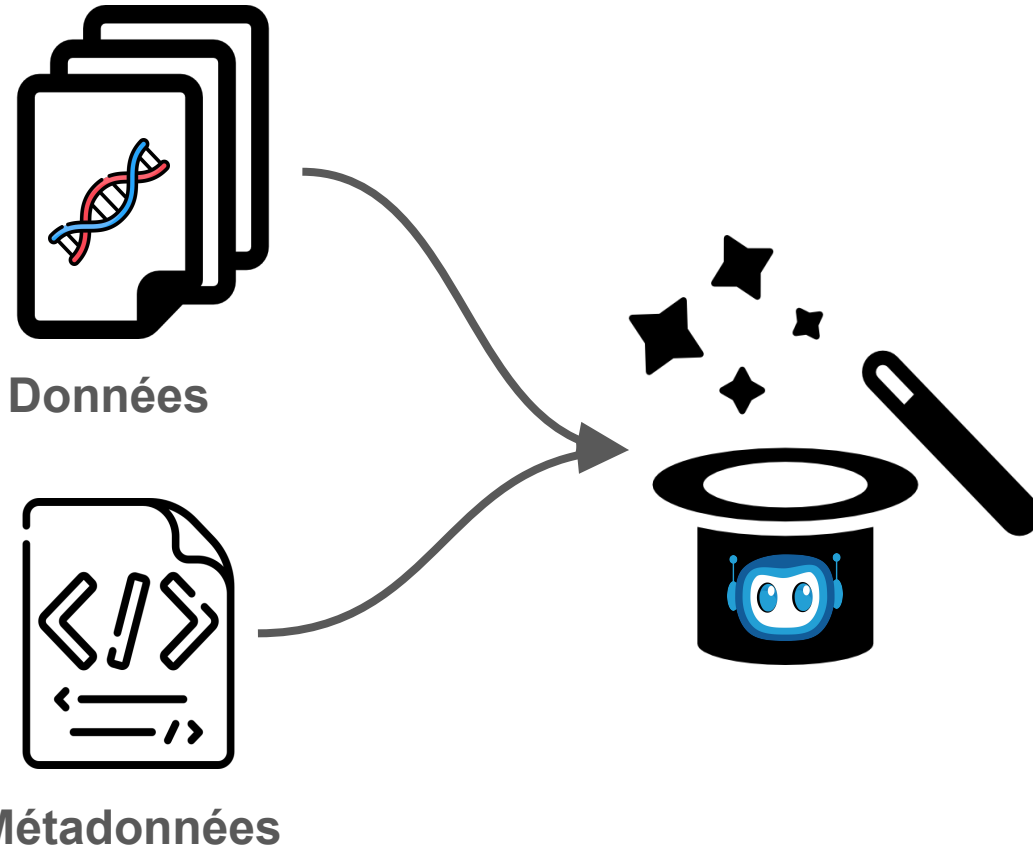
DATALINKS 1 SAMPLES 1 METADATA 3 STUDY 1

[NEW DATALINK](#)

Name	Connections	Data access
NC_045512.2.fasta 29.72 Ko	Galaxy France	Accessible

Items per page: 10 1-1 of 1

Imane Messak





Avec un standard !

In essence, a standard is an **agreed way of doing something**.

A standard provides the **requirements, specifications, guidelines** or **characteristics** that can be used for the **description, interoperability, citation, sharing, publication, or preservation** of all kinds of **digital objects** such as data, code, algorithms, workflows, software, or papers.

source : <https://fairsharing.org/educational/>

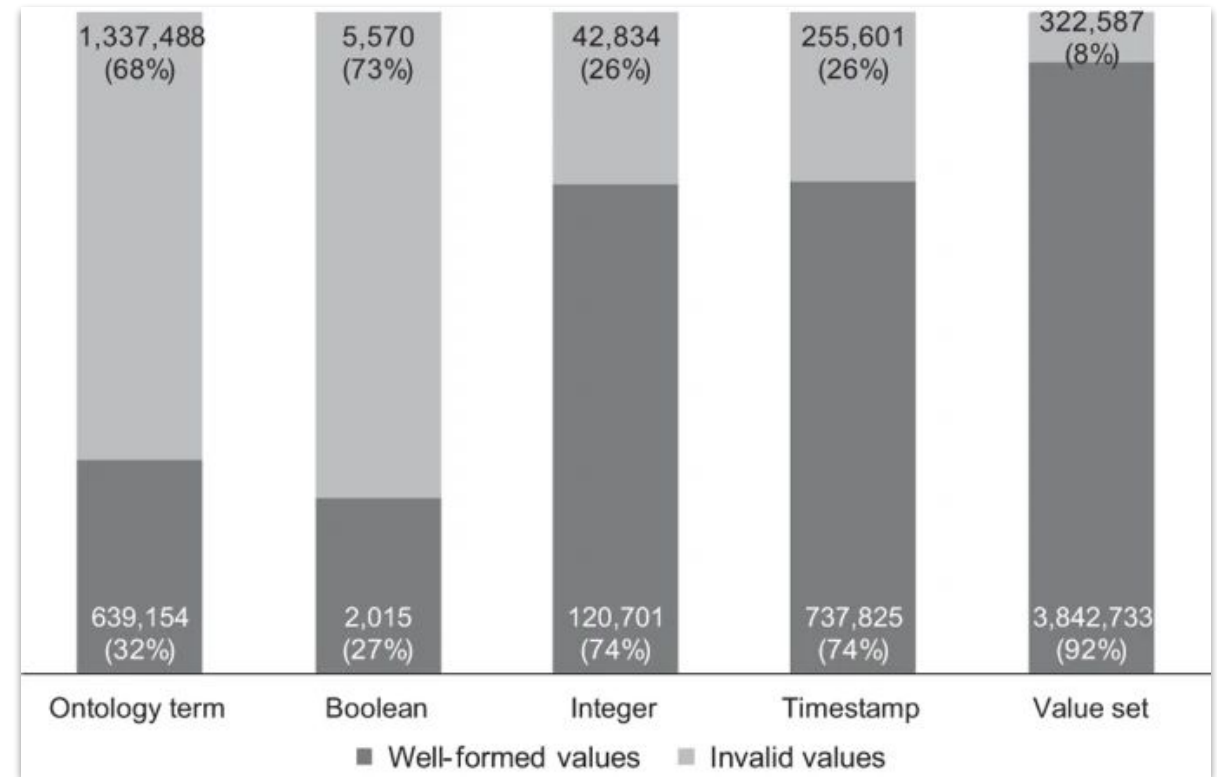


Avec un standard ! Oui, mais...

La soumission à des entrepôts internationaux est souvent une tâche complexe

Les procédures de soumission sont hétérogènes.

Les métadonnées sont souvent incomplètes, incohérentes, redondantes ou insuffisamment informatives.

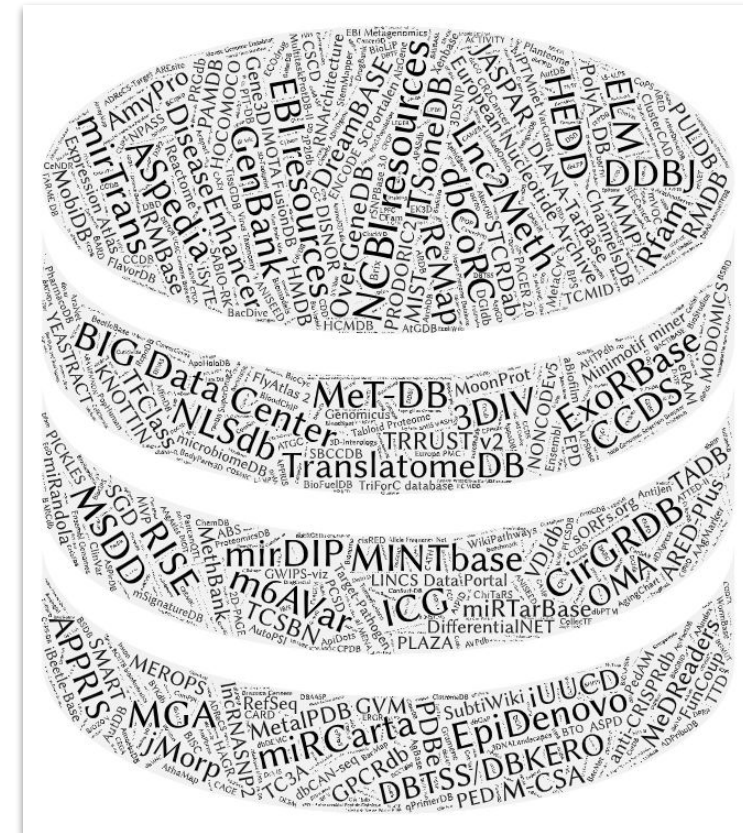


Quality of dictionary attributes in NCBI BioSample according to their type, in [Gonçalves et al., 2019](#)



Il existe des milliers de bases de données, de logiciels et de ressources en biologie dont le niveau **d'adoption des standards est inégal.**

Il n'est pas toujours facile pour les biologistes et les bioinformaticiens d'identifier et d'utiliser les normes appropriées...

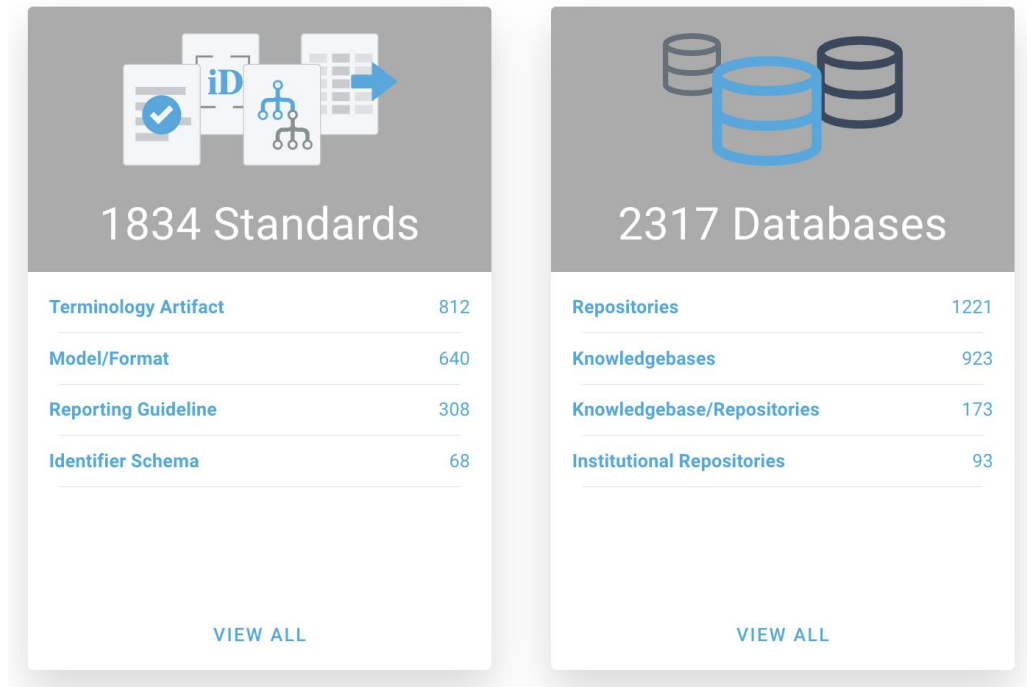


1641 databases in NAR Database 2021

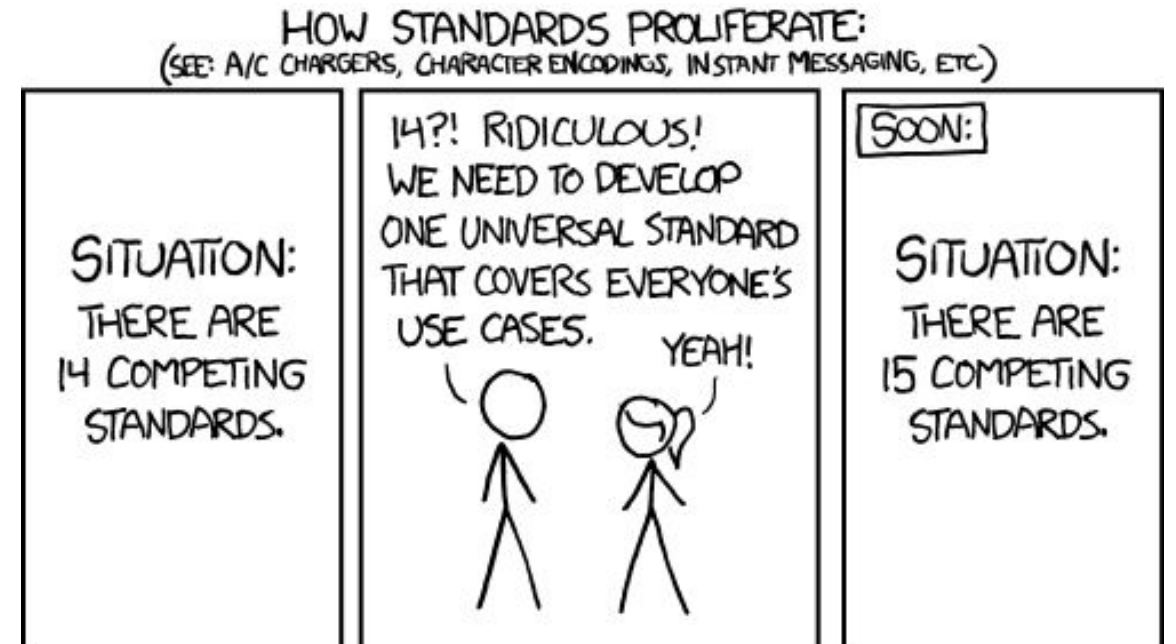
[Rigden et al, 2021](#)



Nous ne sommes pas seuls !



Source : [FairSharing](#)



Source : <https://xkcd.com/927/>

Quels sont les standards à notre disposition ?

- Pour l'**ENA**, les checklists

Une checklist définit les métadonnées minimales et optionnelles attendues pour décrire un échantillon biologique

Elles sont basées sur les recommandations du Genomic Standards Consortium (GSC)

La checklist la plus appropriée dépend du type d'échantillon :

<https://www.ebi.ac.uk/ena/browser/checklists>

- Et pour les autres ?

Checklist: ERC000020 ?

GSC MixS plant associated

Genomic Standards Consortium package extension for reporting of measurements and observations obtained from the environment where the sample was obtained. By choosing the environmental package, a selection of fields can be made from a relevant subsets of the GSC terms.

Checklist Fields ?

Filter fields...

Filter by type:

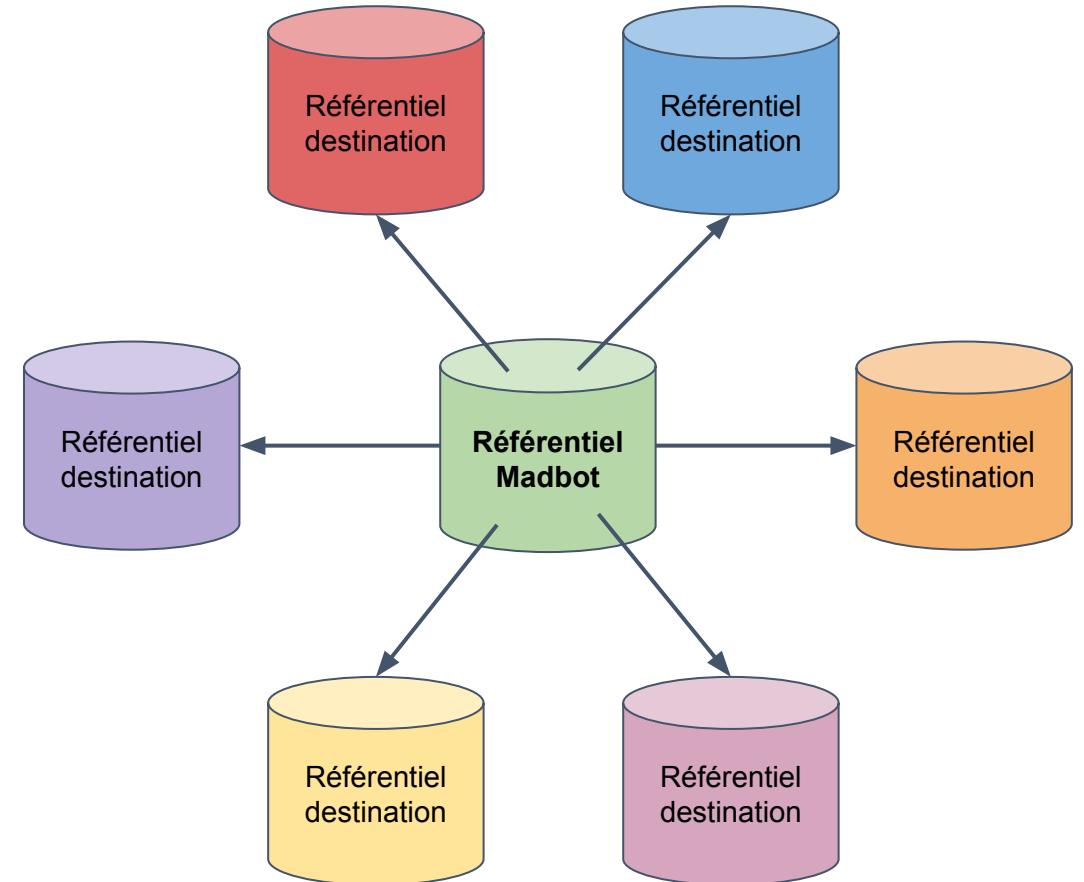
- non-sample terms
- Collection event information
- sample collection
- host disorder
- host description
- local environment conditions
- concentration measurement
- host details
- organism characteristics
- local environment conditions imposed

Field Name	Field Format	(Field Restriction)	Requirement	(Units)
project name	free text		mandatory	
experimental factor	free text		optional	
ploidy	free text		optional	
number of replicons	restricted text	regular expression	optional	
extrachromosomal elements	restricted text	regular expression	optional	
estimated size	restricted text	regular expression	optional	
reference for biomaterial	free text		optional	
annotation source	free text		optional	
sample volume or weight for DNA extraction	restricted text	regular expression	optional	options
nucleic acid extraction	free text		optional	
nucleic acid amplification	free text		optional	
library size	restricted text	regular expression	optional	
library reads sequenced	restricted text	regular expression	optional	

Compte tenu de la grande diversité des standards de métadonnées et de leur faible interopérabilité, nous avons fait le choix de créer un référentiel de métadonnées propres à Madbot.

Ce référentiel jouera le rôle de langage universel pour saisir l'ensemble des métadonnées au sein des arborescences de *Node*, *Sample* et *Data* de Madbot.

Si un lien n'existe pas entre le référentiel de destination et le référentiel Madbot, le champ de destination est malgré tout utilisable.





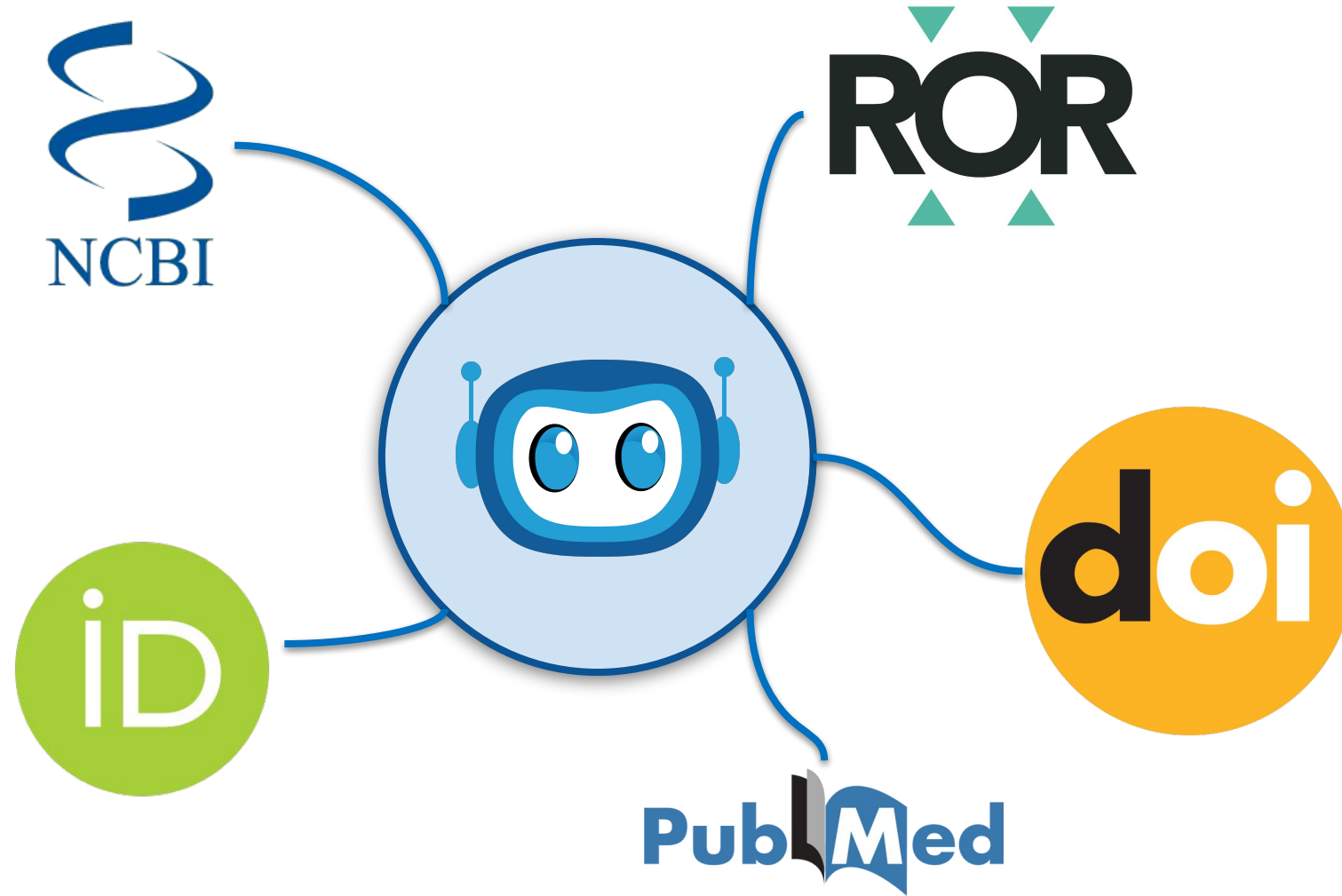
Des métadonnées peuvent être associées aux *Nodes*, *Samples*, *Data* et associations entre *Data*

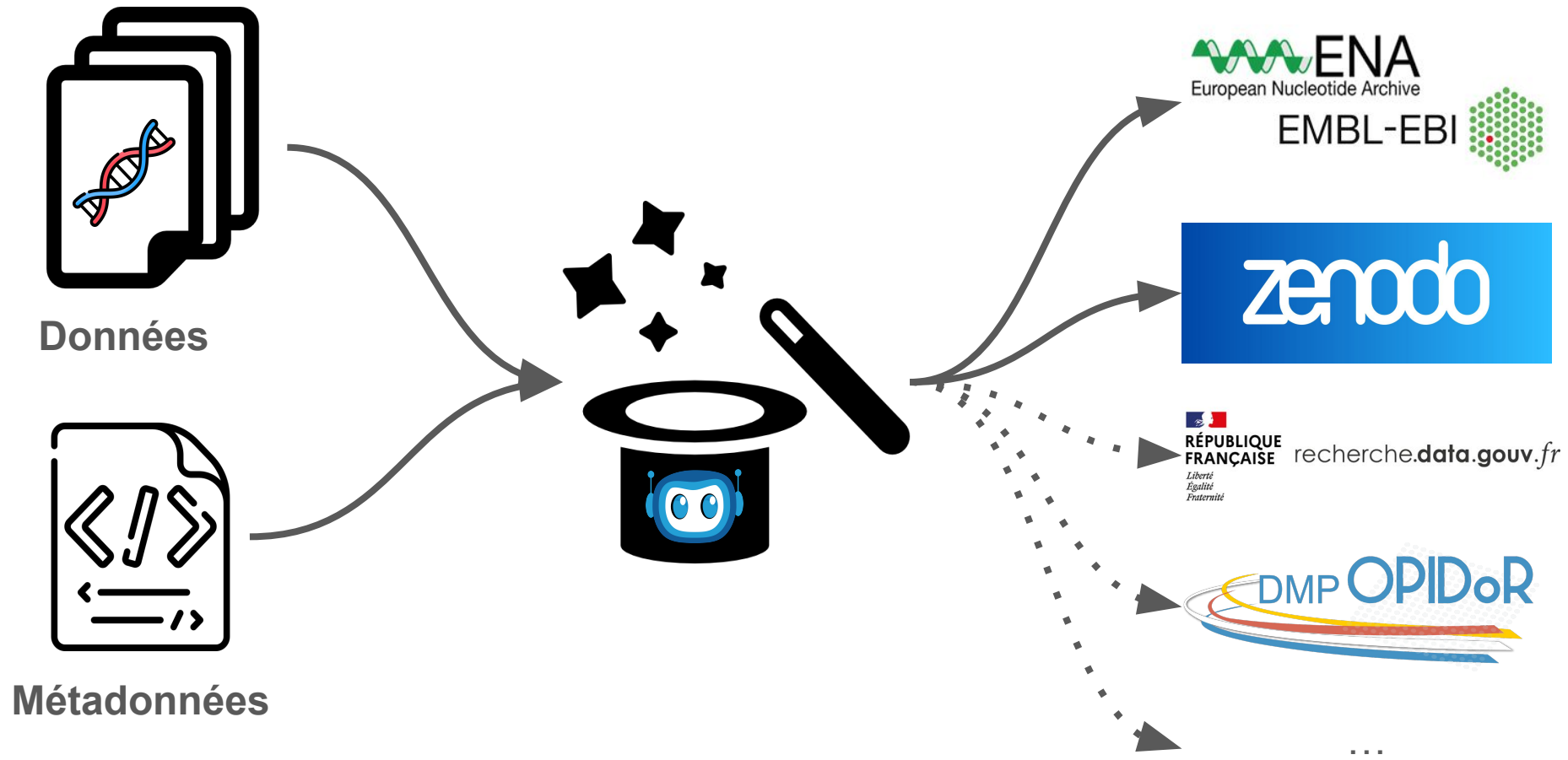


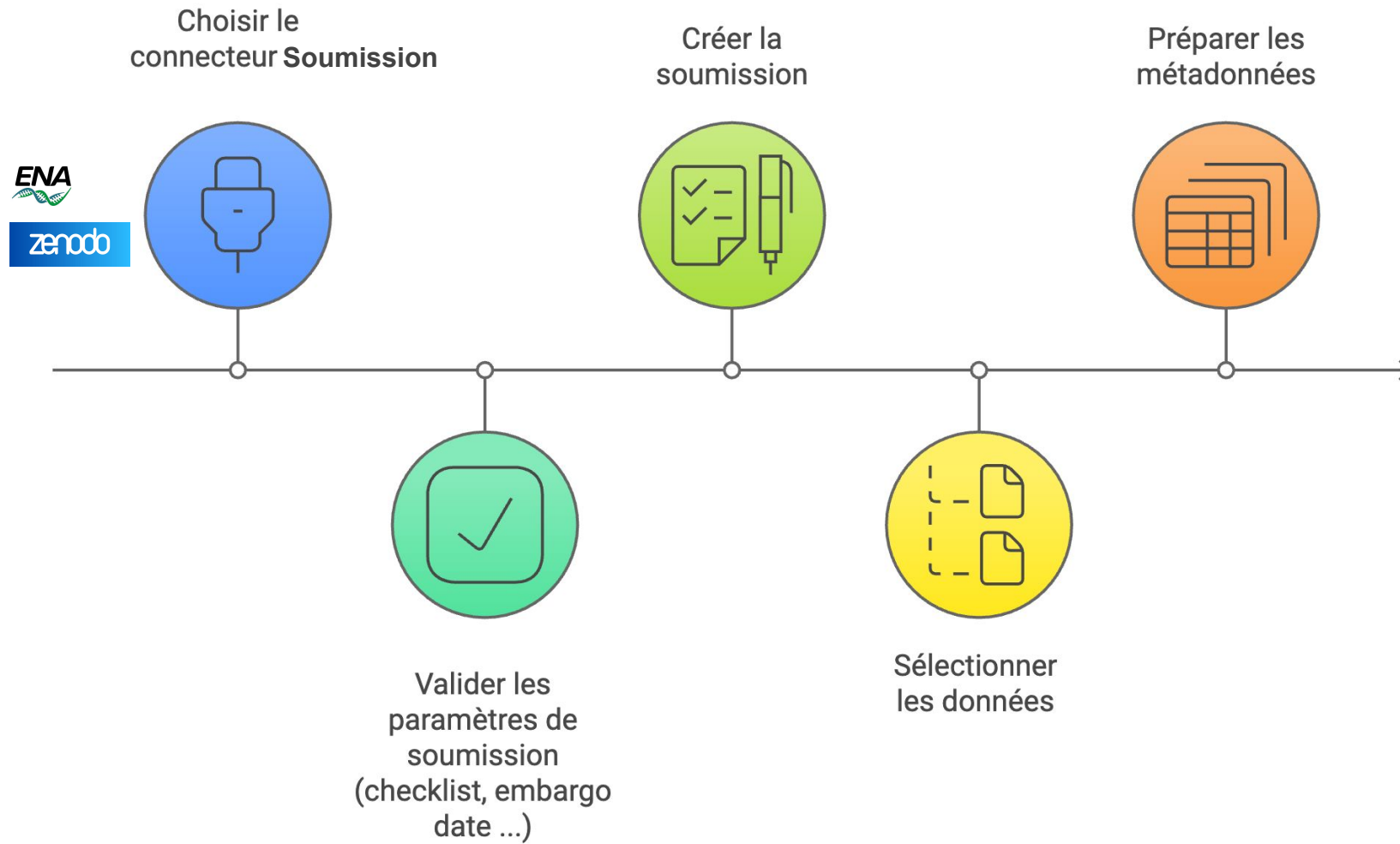
Des métadonnées peuvent être associées aux *Nodes*, *Samples*, *Data* et associations entre *Data*

The screenshot displays the MADBOT interface for a study titled "Growth control of the eukaryote cell: a systems biology study in yeast". The interface includes a sidebar with navigation options like Dashboard, Inbox, Parameters, Submissions, and New investigation. The main content area shows the study title, a brief background description, and a metadata form. The form has tabs for DATALINKS, SAMPLES, METADATA, and STUDY. A validation error message is visible: "- Taxon: must have required property 'taxonID'" and "- Taxon: must have required property 'scientificName'". The form fields include Library name, Sample cell type, Environmental sample, Taxon (with Scientific Name, Taxon ID, and Common Name sub-fields), and a pagination bar at the bottom.

Field	Value
Library name	Growth Control Systems Biology Study Yeast Library
Sample cell type	eukaryote
Environmental sample	<input checked="" type="checkbox"/>
Taxon	Scientific Name* is a required property Taxon ID* is a required property Common Name









MADBOT beta

DEMO - YEAST GROWTH CONTROL

- Dashboard
- Inbox 9
- Parameters
- Submissions
- New investigation

Growth control of the eukaryote cell: a ...

- Study of the impact of changes in fl...

Growth control of the eukar... Everything saved

Growth control of the eukaryote cell: a systems biology study in yeast

investigation

Background Cell growth underlies many key cellular and developmental processes, yet a limited number of studies have been carried out on cell-growth regulation. Comprehensive studies at the transcriptional, proteomic and metabolic levels under defined controlled conditions are currently lacking. Results Metabolic control analysis is being exploited in a systems biology study of the eukaryotic cell. Using chemostat culture, we have measured the impact of changes in flux (growth rate) on the transcriptome, proteome, endometabolome and exometabolome of the yeast *Saccharomyces cerevisiae*. Each functional genomic level shows clear growth-rate-associated trends and discriminates between carbon-sufficient and carbon-limited conditions. Genes consistently and significantly upregulated with increasing growth rate are frequently essential and encode evolutionarily conserved proteins of known function that participate in many protein-protein interactions. In contrast, more unknown, and fewer essential, genes are downregulated with increasing growth rate; their protein products rarely interact with one another. A large proportion of yeast genes under positive growth-rate control share orthologs with other eukaryotes, including humans. Significantly, transcription of genes encoding components of the TOR complex (a major controller of eukaryotic cell growth) is not subject to growth-rate regulation. Moreover, integrative studies reveal the extent and importance of post-transcriptional control, patterns of control of metabolic fluxes at the level of enzyme synthesis, and the relevance of specific enzymatic reactions in the control of metabolic fluxes during cell growth. Conclusion This work constitutes a first comprehensive systems biology study on growth-rate control in the eukaryotic cell. The results have direct implications for advanced studies on cell growth, in vivo regulation of metabolic fluxes for comprehensive metabolic engineering, and for the design of genome-scale systems biology models of the eukaryotic cell.

DATALINKS 1 SAMPLES 1 METADATA 3 STUDY 1

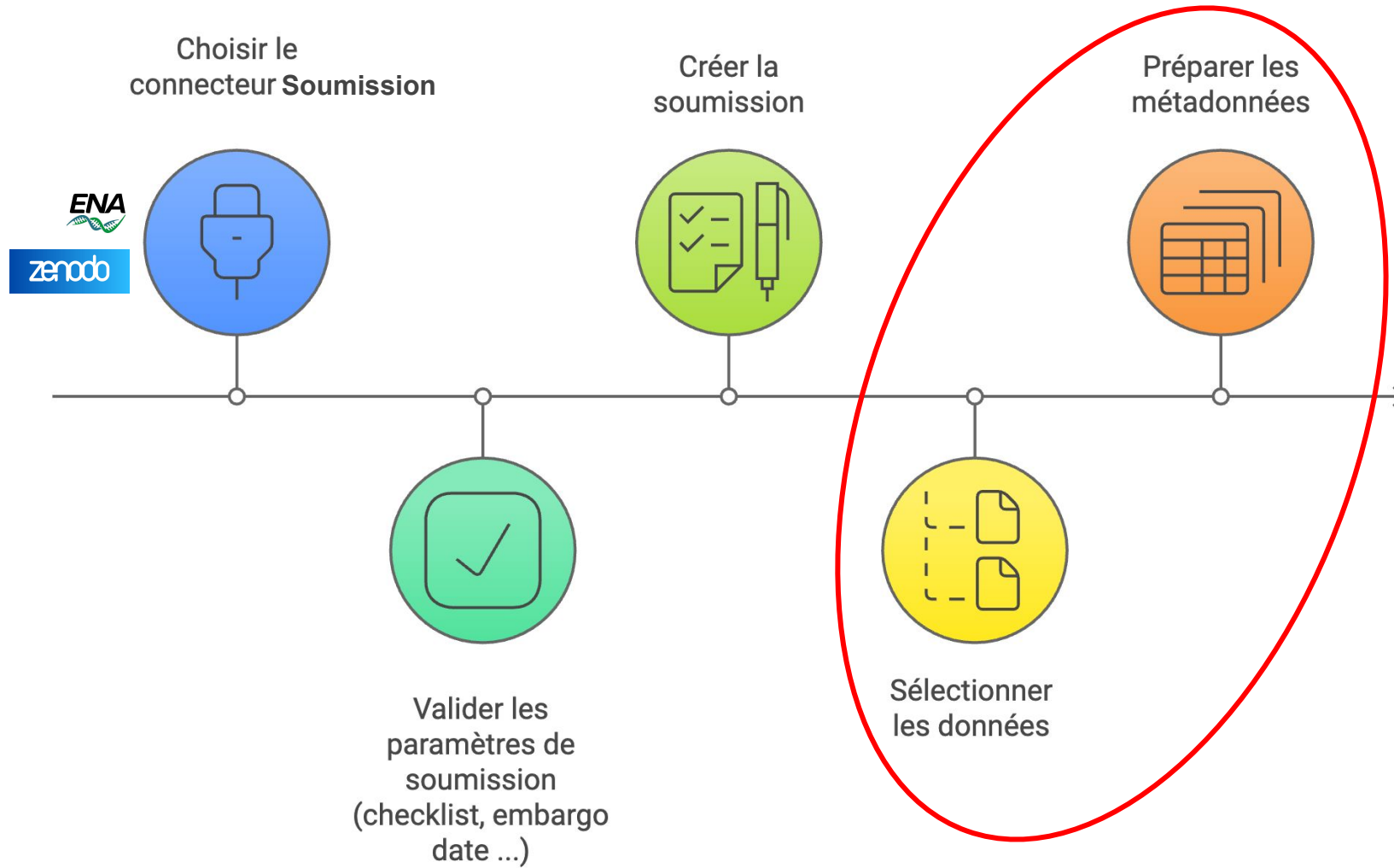
[NEW DATALINK](#)

Name	Connections	Data access
R2.fastq.gz 78.00 octets	core.cluster.france-bioinformatique.fr	Accessible

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Imane Messak

Mattermost



Processus de soumission - Exemple de l'ENA

Sélectionner
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File explorer

Demo - Yeast Growth Control Systems... / Growth control of the eukaryote cel... / Study of the impact of changes in f...

Nodes: Growth control of the euk... | Study of the impact of ch... | protein expression profil...

Data: R2.fastq.gz | proteins.csv

Study of the impact of changes in flux on the transcriptome, proteome, endometabolome and exometabolome of the yeast *Saccharomyces cerevisiae* under different nutrient limitations

study

We wished to study the impact of growth rate on the total complement of mRNA molecules, proteins, and metabolites in *S. cerevisiae*, independent of any nutritional or other physiological effects. To achieve this, we carried out our analyses on yeast grown in steady-state chemostat culture under four different nutrient limitations (glucose, ammonium, phosphate, and sulfate) at three different dilution (that is, growth) rates.

Information

Created time	Tue, 06 May 2025 08:47:51 GMT
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Processus de soumission - Exemple de l'ENA



Sélectionner les données



File explorer

Demo - Yeast Growth Control Systems... / Growth control of the eukaryote cel... / Study of the impact of changes in f...

Nodes

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DATA **1** STUDY SAMPLE RAW READ

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SAVE | Search

Field	Value
Title*	Growth control of the eukaryote cell: a systems biology study in yeast Candidate values: Growth control of the eukaryote cell: a systems...
Alias*	growth-control-of-the-eukaryote-cell-a-systems-biology-study-in-yeast Candidate values: growth-control-of-the-eukaryote-cell-a-systems-...
Description	Background Cell growth underlies many key cellular and developmental processes, yet a limited number of studies have been carried out on cell-growth regulation. Comprehensive studies at the transcriptional, proteomic and metabolic levels under defined controlled conditions are currently lacking. Results Metabolic control analysis is being exploited in a systems biology study of the eukaryotic cell. Using chemostat culture, we have measured the impact of changes in flux (growth rate) on the transcriptome, proteome, endometabolome and exometabolome of the yeast <i>Saccharomyces cerevisiae</i> . Each functional genomic level shows clear growth-rate-associated trends and discriminates between carbon-sufficient and carbon-limited conditions. Genes consistently and significantly upregulated with increasing growth rate are frequently essential and encode evolutionarily conserved proteins of known function that participate in many protein-protein interactions. In contrast, more unknown, and fewer essential, genes are downregulated with increasing growth rate; their protein products rarely interact with one another. A large proportion of yeast genes under positive growth-rate control share orthologs with other eukaryotes, including humans. Significantly, transcription of genes encoding components of the TOR complex (a major controller of eukaryotic cell growth) is not subject to growth-rate regulation. Moreover, integrative studies reveal the extent and importance of post-transcriptional control, patterns of control of metabolic fluxes at the level of enzyme synthesis, and the relevance of specific enzymatic reactions in the control of metabolic fluxes during cell growth. Conclusion This work constitutes a first comprehensive systems biology study on growth-rate control in the eukaryotic cell. The results have direct implications for advanced studies on cell growth, in vivo regulation of metabolic fluxes for comprehensive metabolic engineering, and for the design of genome-scale systems biology models of the eukaryotic cell. Candidate values: Background Cell growth underlies many key cellu...
Center name*	Center name must be string
Additional metadata	Table with 2 columns: Tag, Value. No data.

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Préparer les
métadonnées



ENA **New ENA submission** Everything saved PARAMETERS SUBMIT

Submission to ENA Ready ↻

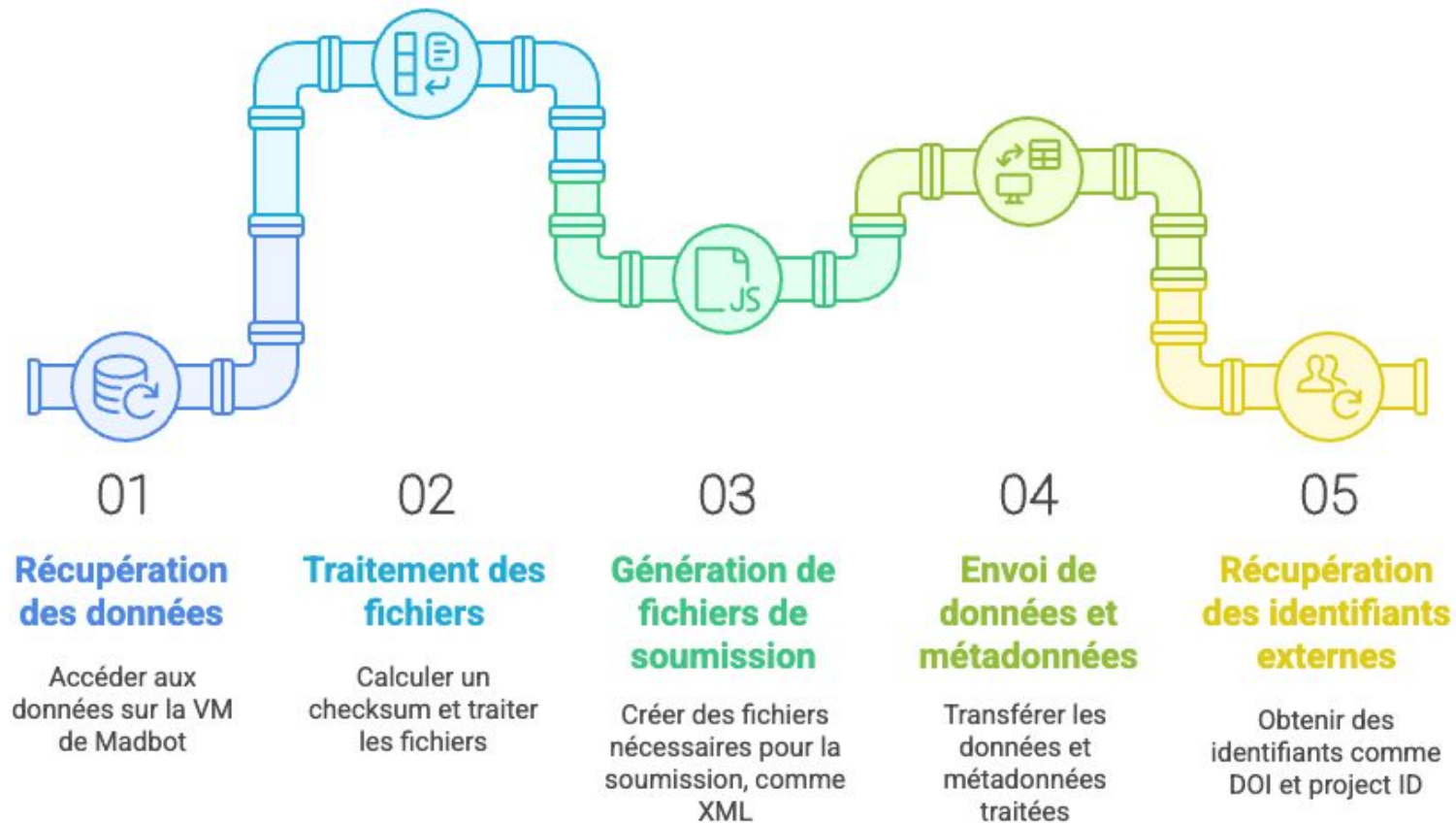
DATA 1 **STUDY** ☀ **SAMPLE** ☀ **RAW READ** ☀

i A raw read object contains the raw sequencing data and information about the sequencing experiment including library and instrument details.


Raw Read Title	Sample Association	Data Association	
raw_read1	sample1	R2.fastq.gz	⋮

Items per page: 10 ▼ 1-1 of 1 << < > >>

Lorsque les données sont associées, les métadonnées renseignées et valides










New ENA submission


Submission to ENA Submitted






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ACCESSION PRJEB89475

DATA **1** STUDY  SAMPLE  RAW READ 

i A raw read object contains the raw sequencing data and information about the sequencing experiment including library and instrument details.

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C'est comment sous le capot ?



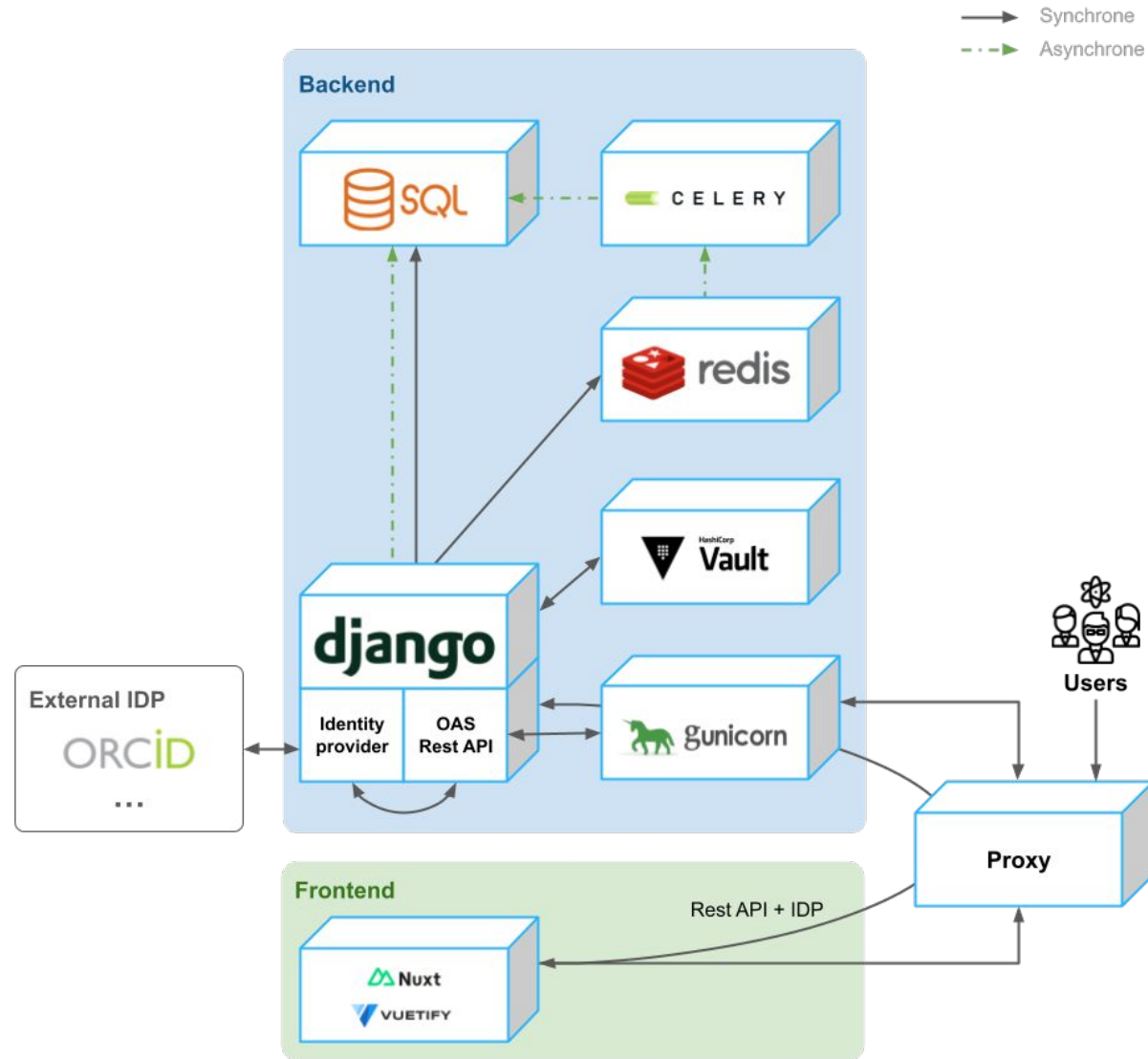
Un projet Open Source sous licence



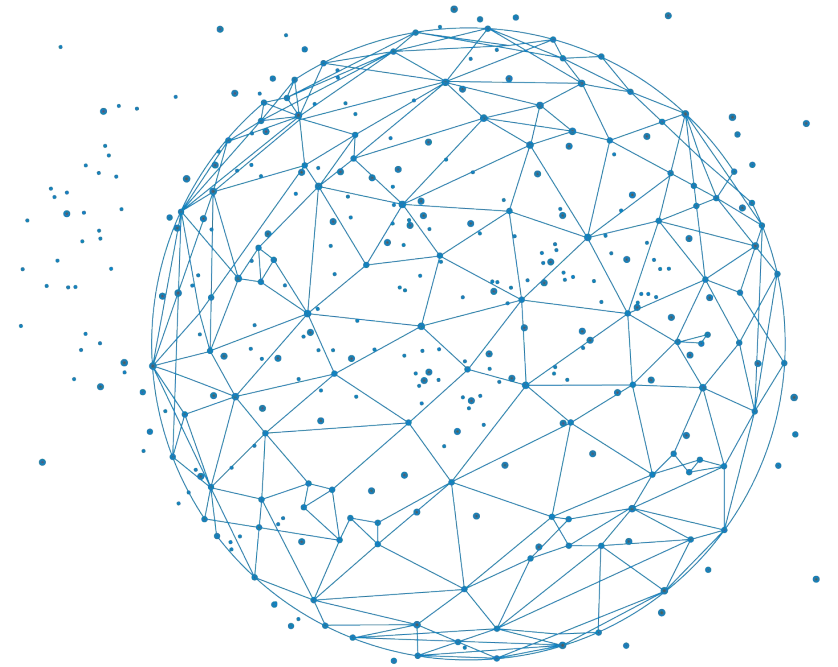
Le **code source** est hébergé sur **Gitlab** : <https://gitlab.com/ifb-elixirfr/madbot>

The screenshot shows the GitLab interface for the 'Madbot' group. At the top, it displays the group name 'Madbot' with a globe icon, a notification bell, and a 'New project' button. Below this, there are tabs for 'Subgroups and projects', 'Shared projects', and 'Archived projects'. A search bar is present, followed by a dropdown menu for sorting by 'Name'. The main content area lists three projects:

Project Name	Description	Stars	Last Update
Madbot API	API of Madbot, the Metadata And Data Brokering Online Tool	3	37 minutes ago
Madbot Client	Web client for Madbot, the Metadata And Data Brokering Online Tool	1	4 days ago
Madbot doc	Documentation for Madbot, the Metadata And Data Brokering Online Tool	3	6 days ago

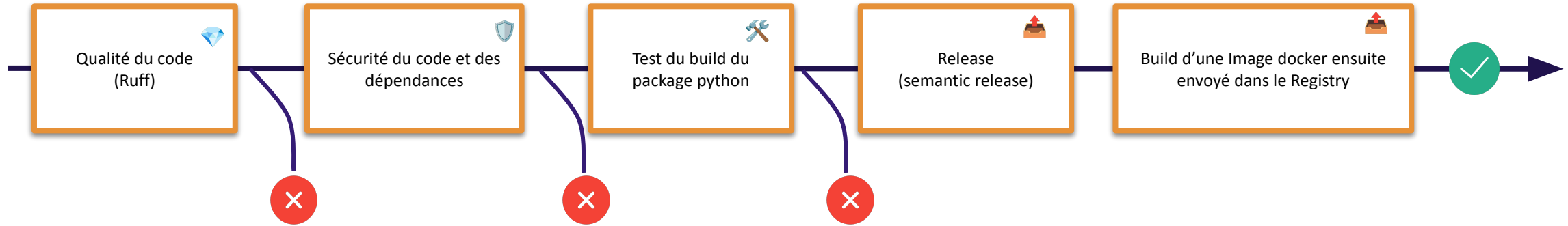


Un projet taillé pour la collaboration

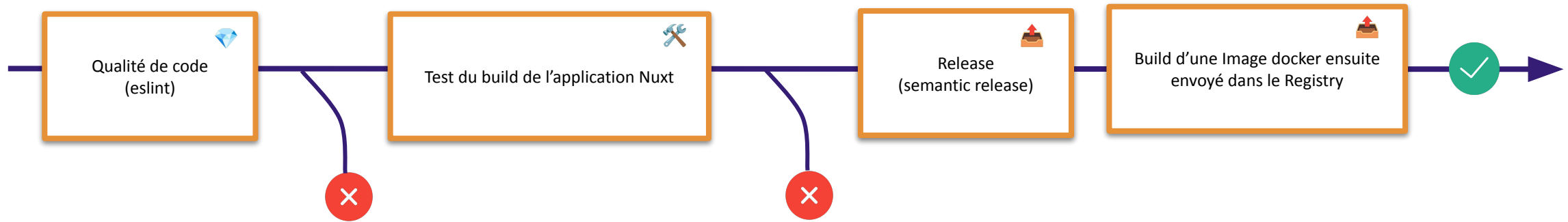




API



Client





Collaboration en cours

- Un groupe de travail se tient toutes les 3 semaines
- Collaboration avec l'action SOI et l'action M2 (Software tools)
- Collaboration avec **Aubii** (UCA) pour la mise en place d'un environnement Docker
- Collaboration avec **FBI** pour la mise en place d'un connecteur IRODS/Omero
- Collaboration avec **Prose** (INRAE) pour la mise en place d'un connecteur DeepOmics

Collaboration à venir

- Collaboration avec l'action M4 (Training) pour la mise en place de formation et d'hackathon
- Et pourquoi pas vous ?





Merci pour votre attention

N'hésitez pas à nous contacter :

contact@france-bioinformatique.fr

